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Figure 1. (SEQ ID NO: 1)

CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC	60
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT	120
AATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTTGAGCGAAGTTTGTGGGGATT	180
TTAGTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAACTGACTTTCATTTGCAACATG	240
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA	300
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG	360
ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCTGCCTTCC	420
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTTTTTTTTTTGGCTTCTTCA	480
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG	540
ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAAACAGAAAT	600
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTA	660
GTTGTGTGTTTGAGGAAAAATAAATGTTTAAGTTGTCCATTCCTTGAAACCTCCCGACC	720
GGG	723



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Figure 2.

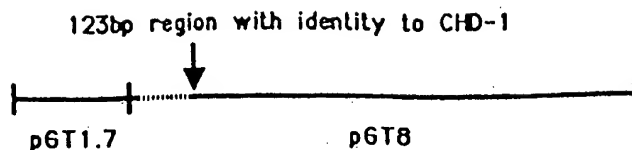


Figure 3.

M	CHD-1	ATTCTTCCAG	ATGATCCTGA	TAAAAACCA	CAAGCAAAC	AGTTACAGAC	(SEQ ID NO: 2)
C	CHD-1A	ATTTTACCTG	ATGATCCAGA	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC	(SEQ ID NO: 3)
C	CHD-W	ATTTTACCTG	ATGATCCAGA	TAAGAAACCC	CAGGCTAAGC	AGTTACAGAC	(SEQ ID NO: 4)
GT	CHD-W	ATTTTACCTG	ATGACCCAGA	TAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC	(SEQ ID NO: 5)

M	CHD-1	CAAAAAACCA	CAAGCAAAC	AGTTACAGAC	CCGTGCAGAC	TACCTCATCA
C	CHD-1A	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC	CCGTGCAGAC	TACCTCATTA
C	CHD-W	CAAGAAACCC	CAGGCTAAGC	AGTTACAGAC	CCGTGCAGAT	TACCTCATTA
GT	CHD-W	CAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC	CCGTGCAGAT	TACCTCATTA

M	CHD-1	AATCTACTAG	CAGAGATCTT	GCAAAAAGAG	AGGCTCAGAG	ACTTTGTGGT	GCG
C	CHD-1A	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAAAG	GCTTGCTGGT	GCA
C	CHD-W	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAGAG	ACTTGCTGGT	GCA
GT	CHD-W	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGTGCAAAG	ACTTACTGGT	GCA

M	CHD-1	ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA	(SEQ ID NO: 6)
C	CHD-1A	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA	(SEQ ID NO: 7)
C	CHD-W	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA	(SEQ ID NO: 8)
GT	CHD-W	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA	(SEQ ID NO: 9)
*****			



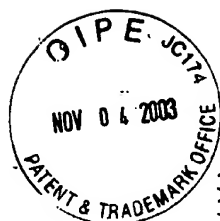
Figure 5.

(SEQ ID NO: 10)

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1 CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG  
51 AAGGCCTGGC CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT  
101 TGGCCATCTG TAGAGAATAG CAAGTCAAAC GCATTACTTC GAAAACATAC  
151 GGAGTACCAG AAAGGGGATT CTTGACCTAC ACCTTGTAAC CTGAGTGGAC  
201 TTTCTTTTAA ACTTCTTAAT ACTTACAATG AATGGGCACA GTGATGAAGA  
251 AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG  
301 GGTGAGCTTC AGGTCTCTGA TCTGGTCAA GCTCTGGAAG CAGTAGCGAT  
351 GGAAGTAGCA GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC  
401 AGGCAGTCAA TCCGAATCAG AGTCTGACAC ATCTAGAGAG AAGAAAACAAG  
451 TTCAAGCTAA ACCTCCGAAA GCTGACGGAT CTGAGTTTGT GAAGTCCAGT  
501 CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA AGCAACAGCA  
551 ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA  
601 GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAAACTAA GAAGAAAAAG  
651 CATAAAGATG AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC  
701 TGGTTCTGAT TCTGAATCGG CGGAAGATGG GGATAAAAGC AGTTGTGAAG  
751 AAAGTGAATC TGACTATGAG CCAAAAAACA AAGTCAAAG CCGTAAACCT  
801 CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG GACAGAAGAA  
851 GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG  
901 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTAG TTACAAAGAA  
951 GCTGAAGAAA CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA  
1001 GGATGTCCCA CAGACTGAAG AAGATGAATT TGAACTATA GAGAAGTTTA  
1051 TGGACAGTCG AATTGGCCGA AAAGGAGCCA CTGGTGCCCT AACCACCATC  
1101 TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG AAAAGTCAAA  
1151 GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA  
1201 TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA  
1251 GGAATGAACA AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG  
1301 CTGGCTGAAA AATGCTTCTC CAGAAGATGT GGAATATTAT AACTGCCAGC  
1351 AGGAGCTTAC AGATGATCTG CACAAACAAT ATCAAATAGT GGAAAGAATA  
1401 ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTATCCGG ACTACTATTG  
1451 CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGCTC  
1501 TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT  
1551 CAATCCAAGA CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC  
1601 AAGATTGTGT GCACTGAAGA AGCAACCATC TTACATTGGA GGACATGAAA  
1651 GTCTGGAGTT AAGAGATTAT CAGTTAAATG GATTGAATTG GCTCGCTCAT  
1701 TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA TGGGTCTGGG  
1751 TAAAACAATA CAAACAATTT CTTTTCTGAA CTACCTGTTT CATGAACATC  
1801 AACTGTATGG CCCTTTTCTT CTGCGCTGTC CACTTCTTAC CTTGACATCT  
1851 TGGCAAAGAG AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTTA  
1901 CTTAGGAGAT ATAACAGTA GAAATATGAT AAGGACTCAT GAATGGATGC  
1951 ATCCACAGAC TAAACGATTA AAGTTAACA TACTTCTGAC GACATATGAA  
2001 ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT GGGCATTCTAT  
2051 AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA  
2101 GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC  
2151 CCACTGCAAA ATTCCTTCAA AGAGCTGTGG TCTTTGTTGC ATTTTCATCAT  
2201 GCCAGAAAAA TTTTCTCCTT GGAAGATTAT TGAAGAGGAG CATGGCAAAG  
2251 GAAGAGAGTA TGGTTATGCA AGTCTTCACA AAGAGCTTGA ACCATTTTAA  
2301 CTAAGAAGAG TTAAAAAAGA TGTAAGAAAG TCTTTACCTG CTAAGGTTGA  
2351 ACAAATCTCG AGGATGGAAA TGAGTGCAAT GCAGAAGCAA TATTACAAGT  
2401 GGATTTTAAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTT AAAAGGCAGT  
2451 ACCTCAGGCT TTCTGAACAT TATGATGGAA CTTAAGAAGT GTTGTAACCA  
2501 TTGCTACCTC ATTAAGCCAC CAGATGATAA TGAATTCTAT AATAAACAGG  
2551 AGGCCTTACA GCATTTGATA CGTAGCAGCG GGAAACTAAT CCTTCTTGAC  
2601 AAGCTACTGA TTCGTCTGCG AGAAGCTGGC AACAGAGTTC TGATTTTCTC  
2651 TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC  
2701 AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG  
2751 CAAGCACTGG ATCATTTCAA TGCAGAAGGA TCAGAGGATT TCTGTTTTTT  
2801 ACTGTCTACA AGAGCTGGAG GATTAGGTAT TAACCTGGCA TCTGCTGACA  
2851 CTGTAGTTAT TTTTGATTCT GACTGGAATC CACAGAATGA TCTGCAGGCA  
2901 CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA ATATTATCG  
2951 GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA



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3001 AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA  
3051 AAAACTGTTC TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA  
3101 TAAAGAAGAG TTATCAGCTA TTTTGAAGTT TGGTGCTGAG GAACTCTTTA  
3151 AAGAACCCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA  
3201 ATCTTGAAGA GAGCTGAAAC TCGGGAAAAAT GAGCCAGGTC CATTGACTGT  
3251 AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG  
3301 ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA  
3351 GAAATCATCC CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA  
3401 AAAAGAACTT GAAGAAATAT ACATGCTCCC GAGGATGAGA AACTGTGCAA  
3451 AACAGATCAG CTTTAATGGG AGTGAAGGAA GACGCAGTAG GAGCAGAAGA  
3501 TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAAC GGCCAAAAAA  
3551 GCGTGGAAAG CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTATGTG  
3601 ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAATT TGGTGGCCCT  
3651 CTGGAAAGGT TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC  
3701 TGAGACAGAC CTTAGACGTT TGGGTGAACT TGTACATAAT GGATGCATTA  
3751 AGGCTTTAAA GGACAATTCA TCTGGACAAG AAAGAGCAGG AGGTAGACTT  
3801 GGGAAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC AGGTGAATGC  
3851 AAAACTAGTC ATCTCTCAGC AAGAAGAGCT GGCACCACTG CACAAATCCA  
3901 TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC  
3951 AAGGCTGCTC ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT  
4001 GTTAGTAGGC ATCTATGAAT ATGGCTATGG CAGCTGGGAA ATGATAAAAA  
4051 TGGATCCAGA TCTCAGCTTA ACACAGAAGA TTTTACCTGA TGATCCAGAC  
4101 AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT ACCTCATTA  
4151 ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAGG CTGCTGGTG  
4201 CAGGCAATTC CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG  
4251 GCTTCAAAAA TAAAAGAAGA AATAAAGAGT GATTCTTCAC CACAACCCTC  
4301 AGAAAAATCT GATGAAGATG ATGAGGAGGA GGATAACAAG GTAAATGAAA  
\*\*

4351 TGAAATCTGA AAATAAGAA AAATCTAAAA AAATTCCATT GCTGGATACT  
4401 CCAGTTTATA TTAAGTCAAC CAGTGAACCA GTTCCTATCT CAGAAGAATC  
4451 TGAAGAATC CATCAGAAGA CATTAGTGT GTGCAAAGAA AGAATGAGGC  
4501 CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGCCTTTCT  
4551 GAAAGGGAGC AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA  
4601 TCACATTACA GAATGCCTGA AGGAGTACAC AAATCCCAG CAAATAAAAC  
4651 AGTGGAGGAA AAATTTGTGG ATTTTGTGT CCAAGTTTAC AGAATTTGAT  
4701 GCCAGAAAGC TGCACAACT CTACAAACAT GCAATCAAAA AGCGCCAAGA  
4751 GTCTCAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG  
4801 TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT  
4851 GATAGTAGCA GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA  
4901 TGATCATCAC AAAGACAGGC ATCAGGGAGA TGCTTACAAG AAAAGTGACT  
4951 CCAGGAAAAG GCCATATTCA GCCTTCAGTA ATGGAAAAGA TCACAGAGAC  
5001 TGGGATCAGT ACAAACAGGA CAGCAGATAC TACAGTGATA GTAAACATAG  
5051 AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA  
5101 ACTTAAAAGA CAGCCGGGGT CATTAGATC ACCGCTCCCA TTCAGACCAC  
5151 AGGATACACT CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC  
5201 TTCGAGAGAT TATAGATACC ACTCAGACTG GCAAAATGGAC CACAGAGCTT  
5251 CTGGTAGTGG CCCGAGGTCA CCACTAGATC AGAGGTCTCC TTATGGTTCA  
5301 AGATCTCCCC TAGGACACAG ATCTCCATTT GAACACTCAT CAGATCACAA  
5351 AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA  
5401 CATTTTCTGG ACCTTCTTTT TAGCCATATA CAGTAAACTA ACACAGTAAT  
5451 TGCCTTACAT GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT  
5501 ATTGTTACTT CTTTCCAGGA TGCAAGGTCT ATTATCCCAA CAGAAGAAAA  
5551 ATATTTTGTG ATTTAAAGTT TATGCTGCAC TGTGCTGCAA ATGTTGTGGC  
5601 ACTTTTTTTT TAAGAAATGG AAGATGTTTA CTTTTACAGG GACCTCAACA  
5651 CTGCCCCCTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG  
5701 TTCTAGGCTG AACACAGATT AAATTATGTT TGTAATGAA CACTTAAACA  
5751 CTGACCTGTG CTTATGTTTC AGGAAAGAAAT GGGGGATTTA TTTTGTTTA  
5801 TTTCTTGGTA GAGAACTCTC AAGGACTTTG TTCACTTTCC AAAGCTACTT  
5851 GTTTACATTG TACACTGCGA CCACCTTGCC GCTTTTCATC ACAAGCTTGA  
5901 ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA TTTCTCCTGT  
5951 TTGTGATCAG TTATAATGCC TTTTATGAA ACAACAAAC AAACAAAAAA  
6001 CAAATAAAAA AAAAAACACA ACAAAACCAA CAAATGGCTG TAAATTATG  
6051 TAAATTAATT AAATGAGCTT TTTTCCGTCA GGCTTTTTTT GGCTGTTCCT  
6101 TTCCCCAACA ACTCAGGCCT TCTTTTCACA AAGTCAGTAT ACTTACATGT  
6151 TTTAATAAAA TATCTCGATG GAATCAGAA GTAAATGAG GGAAGGGGAA  
6201 ATTTTATTCC ATTTAGTCTT CCTTTTTTAT TGGATACTTT TACATACCTG  
6251 TTTTGGTTG TTTTATTTTA TTTTTTTTTT CTATTAAACT GTCAGTGTG  
6301 TGATTGTTGT AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG  
6351 AAAGCTTTTC AGGTGCATTG GTTTAAAAGA AGGAAGTGT CTATAGGTGA



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6401 ACACTTCAAA ACCCAGATCA GCCAAGATTC ATTGTAAATC CATTTGTTTT  
6451 CCCTCTTTAA CATGGGCAAT AATGTCAAAT GTGCTATGCA GCAGTTAATA  
6501 TTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC AATGCACACT  
6551 GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA  
6601 AAAAAACC



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Figure 6.

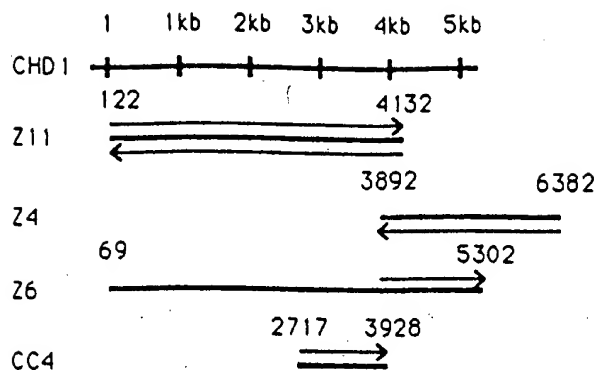


Figure 7.

CHD-1A 1 D E I V S V K H L H K K I K T E (SEQ ID NO: 11)  
CHD-W 1 GATGAGATTGTTTCAGTGAACATCTACATAAAAAATAAAACAGAAA (SEQ ID NO: 12)  
D G I V S V K H P H K K I K A E (SEQ ID NO: 14)

CHD-1A 51 K E N E E K P E P D I G I K K E A  
CHD-W 51 AAAGAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT  
AAAGAAAATGAAGAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT  
K E N E E K D E P E I G I K K E A

CHD-1A 101 E E K R E T K E K E N K R E L K R  
CHD-W 101 GAAGAAAAAGAGAGACAAAAGAGAAAGAAAATAAAAGGGAATTGAAAAGG  
GGAGAAAAAGAGAGACAAAAGAGAAAGGAAAATAAGA  
G E K R E T K E K E N K

CHD-1A 151 E K K E K E D K K E L K E K D N K  
GAGAAAAAGAAAAGAGGATAAGAAAGAATTAAAGAAAAAGATAATAA

CHD-1A 201 E K R E N K V K E S T Q K E K E V  
GAAAAGAGAGAAAACAAAGTAAAGAATCCACACAGAAAGAAAAGAAGTG

CHD-1A 251 K E E K  
AAGGAAGAGAAG



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Figure 8. (SEQ ID NO: 15)

ATTTATCGGC	TAGTCACAAA	AGGATCAGTA	GAAGAAGATA	TTCTTGAAAG	AGCCAAGAAA	AAGATGGTGT	TAGATCATTT
10	20	30	40	50	60	70	80
AGTGATTGAG	AGAATGGACA	CCACAGGGAA	AACTGTACTA	CATACAGGCT	CTACTCCTTC	AAGCTCAACA	CCTTTTAATA
90	100	110	120	130	140	150	160
AGGAAGAGTT	ATCAGCAATT	TGAAGTTTG	GTGCTGAGGA	ACTTTTAAAA	GAACCTGAAN	NNGAAGAAGA	GGAGCCTCAG
170	180	190	200	210	220	230	240
GAGATGGATA	TAGATGAAAT	OCTGAAGAGG	NCTGAAACTC	GAGAAAAATGA	GTGAGGCCCA	TTAACTGTAG	GAGATGAGTT
250	260	270	280	290	300	310	320
ACTTTCACAG	TTCAAGGTAG	CTAACTTTTC	CAATATGGAT	GAAGATGACA	TTGAATTGGA	ACCAGAACAA	AATCTAAGAA
330	340	350	360	370	380	390	400
ACTGGGAAGA	AATCATTCCA	GAAGTTCAGT	GGCGAOGAAT	AGAGGGGNG	GAAAGACAAA	AAGAAGTGA	AGAAATATAT
410	420	430	440	450	460	470	480
ATGCTTCCAA	GAATGAGAAA	CTGTCCAAAA	CAGATCAGCT	TTAATGGAAA	TGAAGGGAGA	TGCAGTAGGA	GCAGAAGATA
490	500	510	520	530	540	550	560
TTCTGGATCT	GATAGTGATT	CCATCTCAGA	AAGAAAACGA	CCAAAAAAC	GTGGACGACC	ACGAAGTATT	CCCCGTGAAA
570	580	590	600	610	620	630	640
ACATTAAGG	ATTTAGTGAT	GCAGAGATTA	GACGATTTAT	CAAGAGTTAC	AAGAAATTTG	GTGGCCCACT	TGAAAGGTTA
650	660	670	680	690	700	710	720
GATGCTATAG	CTAGAGATGC	TGAGCTAGTT	GATAAATCTG	AAACAGACCT	TAGACGCTG	GGAGAAGTTG	TACATAATGG
730	740	750	760	770	780	790	800
ATGCATTAAG	GCTTTAAATG	ATAATGACTT	TGGTCAAGGA	AGAACAGGTG	GTAGATTGG	GAAAGTTAAA	GGCCCAACAT
810	820	830	840	850	860	870	880
TCCGAATAGC	AGGAGTGCAG	GTGAATGCCA	AGCTAGTCAT	TTCTCACGAA	GAAGAGTTGG	CACCATTCGA	TAAATCGATT
890	900	910	920	930	940	950	960
CCTTCAGATC	CAGAAGAAAG	GAAAAGATAT	GTGATCCCAT	ACCACACCAA	AGCAGCTCAT	TTTGATATAG	ATTGGGGTAA
970	980	990	1000	1010	1020	1030	1040
AGAAGATGAT	TCCAATCTGT	TAATAGGCAT	CTATGAATAT	GGTTATGGCA	GTTGGGAAAT	GATAAAAAATG	GATCCTGATC
1050	1060	1070	1080	1090	1100	1110	1120
TCAGTTTGAC	ACAGAAGATT	TTACCTGATG	ATCCAGATAA	GAAACCCAG	GCTAAGCAGT	TACAGACTCG	TGCAGATTAC
1130	1140	1150	1160	1170	1180	1190	1200
CTCATTAAAT	TACTGAATAA	AGACCTTGCA	AGAAAGGAAG	CACAGAGACT	TGCTGGTGCA	GGCAATTCAA	AGAGGAGAAA
1210	1220	1230	1240	1250	1260	1270	1280
AACAAGAACT	AAGAAGAATA	AAGCAACAAA	GGCTGC				
1290	1300	1310					



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Figure 9.

C CHD-1A DARRYLGNLGH\*RIASQTHYFENIRSTRKGILOLHLVT\*VDFLNFLLITMNGHSDDEE (SEQ ID NO: 16)  
M CHD-1 FALCPFVTPQREPQETRECRKFIFEILIFEICITHLLIGDFCFINFLIPTMNGHSDDEE (SEQ ID NO: 17)  
\*\*\*\*\*

C CHD-1A SVRNSSGZSSRSDSDSAGSASGSGSGSSGSSSDGSSSSQSGSSDSZSGSZSGSQSESESD  
M CHD-1 SVRNSSGZSSQSGDD-CGSASGSGSGSGSSGSSSDGSSSSQSGSSDSZSGSZSGSQSESESD  
\*\*\*\*\*

C CHD-1A TSREKKQVQAKPPKADGSEFWKSSPSILAVQSAVLKQOQQ---QKAASSDSGSEZDSS  
M CHD-1 TSRENK-VQAKPPKVDGAZFWKSSPSILAVQSAVLKQOQQOQOQPASSNSGSEZDSS  
\*\*\*\*\*

C CHD-1A SSEDSDSSSETKKKKKKEDWQMSGSGSVSGTGSDESZSAEDGKSSCZESZSDYEPKN  
M CHD-1 SSEDSDSSSGAKKKKEDWQMSGSGSPQLGSDSESZEDRKSSCDGTEZSDYEPKN  
\*\*\*\*\*

C CHD-1A KVKSRKPPSRKPKSGKKSTGQKKRQLDSSEEEEDDEDYDKRGSRRQATVNVSYKEAEZ  
M CHD-1 KVKSRKPPSRKPKSGKKSTGQKKRQLDSSEEEEDDEDYDKRGSRRQATVNVSYKEAEZ  
\*\*\*\*\*

C CHD-1A TKTSDDLLEVCGEDVPQTEDEFETIEKFMDSRIGRKATGASTTIYAVZADGPNAGF  
M CHD-1 MKTSDDLLEVCGEDVPQTEDEFETIEKFMDSRIGRKATGASTTIYAVZADGPNAGF  
\*\*\*\*\*

C CHD-1A KTXEPCZIQYLKWKWGHSHIHTWETEEZTLKQONVRGMKKLDNYKKQDQETKRWLKQAS  
M CHD-1 EKSKELZIQYLKWKWGHSHIHTWETEEZTLKQONVRGMKKLDNYKKQDQETKRWLKQAS  
ERNKEFDIQYLKWKWGHSHIHTWETEEZTLKQONVRGMKKLDNYKKQDQETKRWLKQAS  
\*\*\*\*\*

HUMAN PEDVEYYNCQQLTDDLHKQYQIVERTNXSPQSKSAAGYP (SEQ ID NO: 18)  
C CHD-1A PEDVEYYNCQQLTDDLHKQYQIVERTNXSPQSKSAAGYPDYCKWGLPYSECSWEDGA  
M CHD-1 PEDVEYYNCQQLTDDLHKQYQIVERTNXSPQSKSAAGLPDYCKWGLPYSECSWEDGA  
\*\*\*\*\*

C CHD-1A LIAKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPFRVALKQPSYIGGHEZLELRDYQLN  
M CHD-1 LISKKFQTCIDEYFSRNQSKTTPFKDCKVLKQRPFRVALKQPSYIGGHEZLELRDYQLN  
\*\*\*\*\*

C CHD-1A GLNWLASHWCKGNSCILADEMGLKTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTWSQR  
M CHD-1 GLNWLASHWCKGNSCILADEMGLKTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTWSQR  
\*\*\*\*\*

C CHD-1A EIQTWAPQMNNAVYLGDIISRNMIRTHEWHPQTKRLKFNILLTTYEILLKDKSFLGGLN  
M CHD-1 EIQTWASQMNNAVYLGDIISRNMIRTHEWHPQTKRLKFNILLTTYEILLKDKAFLGGLN  
\*\*\*\*\*

C CHD-1A WAFIGVDEAHLKNDSSLYRTLIDFKSNERLLITGTPLOSLKELWSLLEFIMPEKFS  
M CHD-1 WAFIGVDEAHLKNDSSLYRTLIDFKSNERLLITGTPLOSLKELWSLLEFIMPEKFS  
\*\*\*\*\*

C CHD-1A WEDFEEZHGKREYGYASLEKELEPFLRRVVKDVEKSLPAKVEQILRMZMSALQKQYK  
M CHD-1 WEDFEEZHGKREYGYASLEKELEPFLRRVVKDVEKSLPAKVEQILRMZMSALQKQYK  
\*\*\*\*\*

C CHD-1A WILTRNYKALSKSGSGSTSGFLNIMZLKKCCNHCYLIKPPDDNZFYNKQZALQHLIRSS  
M CHD-1 WILTRNYKALSKSGSGSTSGFLNIMZLKKCCNHCYLIKPPDDNZFYNKQZALQHLIRSS  
\*\*\*\*\*

C CHD-1A GKLILLDKLLIRLRERGNRVLIFSQVVRMLDI LAEYLYKQYQFPFQRLDGSIKGELRKQAL  
M CHD-1 GKLILLDKLLIRLRERGNRVLIFSQVVRMLDI LAEYLYKQYQFPFQRLDGSIKGELRKQAL  
\*\*\*\*\*





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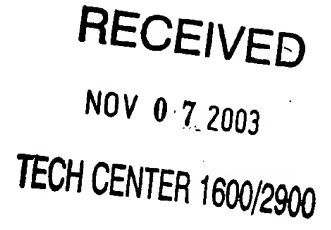
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C CHD-1A  
M CHD-1DBFNAEGSEDFCFLLSSTRAAGGLGINLASADTVVIFDSWNPQNDLQAQARAERIGQKQV  
DBFNAEGSEDFCFLLSSTRAAGGLGINLASADTVVIFDSWNPQNDLQAQARAERIGQKQV  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1-IYRLVTKGSVEEDILERAQKKMVLHDLVIOQMDTTGKTVLBTGSTPSSSTPPNKEELSA (SEQ ID NO: 19)  
NIYRLVTKGSVEEDILERAQKKMVLHDLVIOQMDTTGKTVLBTGSTPSSSTPPNKEELSA  
NIYRLVTKGSVEEDILERAQKKMVLHDLVIOQMDTTGKTVLBTGSTPSSSTPPNKEELSA  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1ILKFGAEELFKPEPEXEEZEPQEMDIDEILKRAETRENESGPLTVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEZEPQEMDIDEILKRAETRENEPGPLSVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEZEPQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNM  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1DEDDIELEPEQNLRNWEIIPPEVQWRRIEGKERQKELEIYMLPRMRNCAQDISFNGNEG  
DEDDIELEPERNSKNWEIIPPEQRRLEKEERQKELEIYMLPRMRNCAQDISFNGSEG  
DEDDIELEPERNSRNWEIIPESQRRRIEKEERQKELEIYMLPRMRNCAQDISFNGSEG  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1RCSRSRYSGSSDSISERKRPKRGPRPTIPRENIGFSDAEIRRFIKSYKPGGPVER  
RRSRSRYSGSSDSISERKRPKRGPRPTIPRENIGFSDAEIRRFIKSYKPGGPVER  
RRSRSRYSGSSDSISERKRPKRGPRPTIPRENIGFSDAEIRRFIKSYKPGGPVER  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1LDALARDAEVLVDKSETDLRLRGLZLVHNGC IKALNDNDFOQGRTOGRFGKVGKPTFRLAGV  
LDALARDAEVLVDKSETDLRLRGLZLVHNGC IKALNDNDFOQGRTOGRFGKVGKPTFRISGV  
LDALARDAEVLVDKSETDLRLRGLZLVHNGC IKALNDNDFOQGRTOGRFGKVGKPTFRISGV  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1QVNAKLVISHEEELAPLEKSIPSDPEERKRYVIPYHTKAABFDIDWGKEDDSNLLIGIYE  
QVNAKLVLAEDELIPLEKSIPSDPEERKRYVIPYHTKAABFDIDWGKEDDSNLLIGIYE  
QVNAKLVISHEEELAPLEKSIPSDPEERKRYVIPYHTKAABFDIDWGKEDDSNLLIGIYE  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1YGYGSWEMIKMDPDLSTQKILPDDPKKPOAKQLOTRADYLIKLLNKDLARKEAQRLAG  
YGYGSWEMIKMDPDLSTQKILPDDPKKPOAKQLOTRADYLIKLLNKDLARKEAQRLAG  
YGYGSWEMIKMDPDLSTQKILPDDPKKPOAKQLOTRADYLIKLLNKDLARKEAQRLAG  
\*\*\*\*\*C CHD-W  
C CHD-1A  
M CHD-1AGNSKRRKTRSKQKATKAA  
AGGSKRRKTRAKSKAKKSIVKZEIKSDSSPLPSEKSDDEDD---KLNDSKPESKDRS  
AGNSKRRKTRKQK-KKASKIKZEIKSDSSPQSEKSDDEDDDEEDNKVNEHKSSENKKS  
\*\*\*\*\*C CHD-1A  
M CHD-1KKSVSDAPVHITASGEFVPIAESEELDQKTFISICKERMRPVKAALKQLDRPEKGLSER  
KKIPLDTPVHITATSEKVPVISESEELBQKTFISVCKERMRPVKAALKQLDRPEKGLSER  
\*\*\*\*\*C CHD-1A  
M CHD-1EQLEHTRQCLIKIGDHITELCKEYSNPEQIKQWRQNLWIFVSKTFEDARKLEKLYKHA  
EQLEHTRQCLIKIGDHITELCKEYSNPEQIKQWRQNLWIFVSKTFEDARKLEKLYKHA  
\*\*\*\*\*C CHD-1A  
M CHD-1KKRQESQONSDQN-SNVATTHVIRNPDMERLKEZTNHDDSSRDSYSSDRHLSQYHDHKKD  
KKRQESQONSDQN-SNVATTHVIRNPDMERLKEZTNHDDSSRDSYSSDRHLSQYHDHKKD  
\*\*\*\*\*C CHD-1A  
M CHD-1REQGDYKKSDSRKPYSFSSNGKDHREWDHYRQDSRYSDREKRLDDHRSREHRPSL  
REQGDYKKSDSRKPYSFSSNGKDHREWDHYRQDSRYSDS-KERLDDHRSRDHRSNL  
\*\*\*\*\*C CHD-1A  
M CHD-1EGGLKD-RCHSDHRSBHDHRSBHDHRSSTPSTHINPFRDYRLSDWQDLHRAASSGPRSP  
EGNLKDSRGHSDHRSBHDHRSBHDHRSSTPSTHINPFRDYRLSDWQDLHRAASSGPRSP  
\*\*\*\*\*C CHD-1A  
M CHD-1LDQRSPYGSRSF-----FEBSAEHRSTPEHTWSSRKTQKLSLSSGTLFXP  
LDQRSPYGSRSPLGHRSPFEHSSDEKSTPEHTWSSRKTQKLSLSSGTLFXP  
\*\*\*\*\*C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1ALTXLERYGLDILSVAVLLLSRMQGLLSQKQKIFVFKVYAALCKCCGTTFLRNGRCLL  
LQGPQBCPFQGTGSYYKTLFVKVVLGXTQIKLCIXMNTXLTCAVSGKNGGFIIFYFLVE  
NSQGLCSLSKATCLECTLRPPCRFSSQAXIFKFTYSCKLARISFVCDQLXCLFHKQTNK  
QKTIKKQNTTKPTNCKLLXINXMSFPFSGFWLFLSPTTQAPFSQSQYTYHFXQNISME  
SECKNGEIGNILFBLVLLPYWILLHTCFWLFYFIFYFYXTVSVVIVVHNSENIPLXTVPWK  
AFQVWTKRKCSIGZBFKQISQDSLXTHLFLSLFMGNNVKCAHQQLIFKXIXMTLLTE  
LLQCTLIVERXLLSDKLNXLKPKT





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Figure 11.

CCHD	AVEAD	GDPNAGFEKSKELGE.IQYLIKWGWSHIENTWETEET	LKQONVKGHNKLDNYKK (SEQ ID NO: 22)
MCHD	AVEAD	GDPNAGFERNKEPGD.IQYLIKWGWSHIENTWETEET	LKQONVRGNKRLDNYKK (SEQ ID NO: 23)
YCHD	EGRVL	EKTVPDLNNCKE..N.YEFLIKWTOESHLNTWETYES	IGQ..VRGLKRLDNYCK (SEQ ID NO: 24)
		**          ****    **     *****	*   *   *     ****   *
DHP1	EEEE	YAVEKIIDRRVRK GK.VEYYLKWKGYPETENTWEPENN	LDCQDLIQY (SEQ ID NO: 25)
BHP1	EDEE	YVVEKVLDRRVVKGQVEYLLKWKGFSEEHNTWEPEKN	LDCPELISEF (SEQ ID NO: 26)
MMOD1	EEEE	YVVEKVLDRRVVKGK.VEYLLKWKGFSDONTWEPEEN	LDCPDLIAEF (SEQ ID NO: 27)
MMOD2	AEPEE	FVVEKVLDRRVVNGK.VEYFLKWKGFTDADNTWEPEEN	LDCPELIEDF (SEQ ID NO: 28)
	**	***     *****    **     *****	***     **
DPC	PVDLV	YAAEKIIQKRVKGV.VEYRVKWKGNQRYNTWEPENN	ILDRRLIDIY (SEQ ID NO: 29)
MMOD3	VGEQV	FAAECILSKRLRK GK.LEYLVKWRGWSSKHNSWEPEEN	ILDPRLLLAF (SEQ ID NO: 30)
	*	***     **     *****    **     *****	*****
		**          **          **     **	



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Figure 14.

MOUSE	CHD1	AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA	(SEQ ID NO: 31)
CHICKEN	CHD-1A	--- --- --- --- --- --- ---C ---C ---A-A ---	(SEQ ID NO: 32)
SPIX	CHD-1A	--- --- --- --- --- --- ---C ---C --- ---	(SEQ ID NO: 33)
CHICKEN	CHD-W	--- --- --- --- --- --- ---C ---A ---	(SEQ ID NO: 34)
SPIX	CHD-W	--- --- --- --- --- --- ---C ---A ---	(SEQ ID NO: 35)
HYACINTH	CHD-W	--- --- --- --- --- --- ---C ---A ---	(SEQ ID NO: 36)
P1		A TAT TCT GGA TCT GAT AGT GAY TC	(SEQ ID NO: 37)
P3		AGA TAT TCC GGA TCT GAT AGT GA	(SEQ ID NO: 38)
MOUSE	CHD1	AGG AAA <u>CGG CCG</u> AAG AAA CGT GGG CGA CCC CGC ACT	
CHICKEN	CHD-1A	--A --- ---A --A --G --- --A A-- --T --A --C	
SPIX	CHD-1A	--- --- ---A --A --G --- --A A-- --A --A ---	
CHICKEN	CHD-W	--A --- --A --A --A --- --- --A --- --A --A ---	
SPIX	CHD-W	--A --- --A --A --GA --- --- --A --- --A --A ---	
HYACINTH	CHD-W	--A --- --A --A --GA --- --- --A --- --A --A ---	
MOUSE	CHD1	ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG	
CHICKEN	CHD-1A	--T --- --A --A --- --- --- --- --- ---A ---	
SPIX	CHD-1A	--T --- --A --A --- --A --- --- --- --- ---	
CHICKEN	CHD-W	--T --C --T --A --C --- --- --- --- ---A ---	
SPIX	CHD-W	--T --- --T --A --- --- --- --- --- ---	
P2		TTT CCT AAA TCG CTA CGT CT	(SEQ ID NO: 39)
HYACINTH	CHD-W	--- --- --- --- --- --- ---C --- --A --G	
HYACINTH	CHD-W	ATT AGG CGG T	